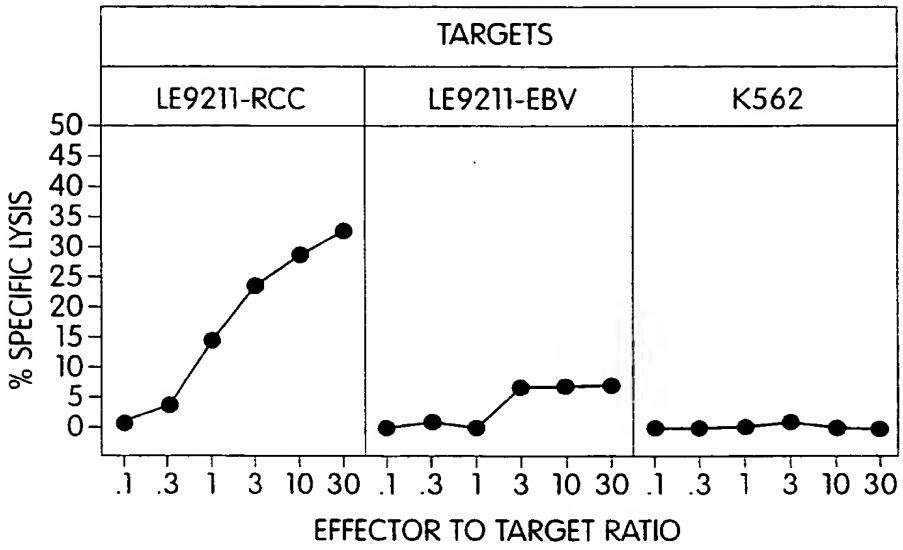
TARGETS
LE9211-RCC
LE9211-EBV
K562
% SPECIFIC LYSIS
50
45
40
35
30
25
20
15
10
5
0
.1 .3 1 3 10 30 .1 .3 1 3 10 30 .1 .3 1 3 10 30
EFFECTOR TO TARGET RATIO

Fig. 1

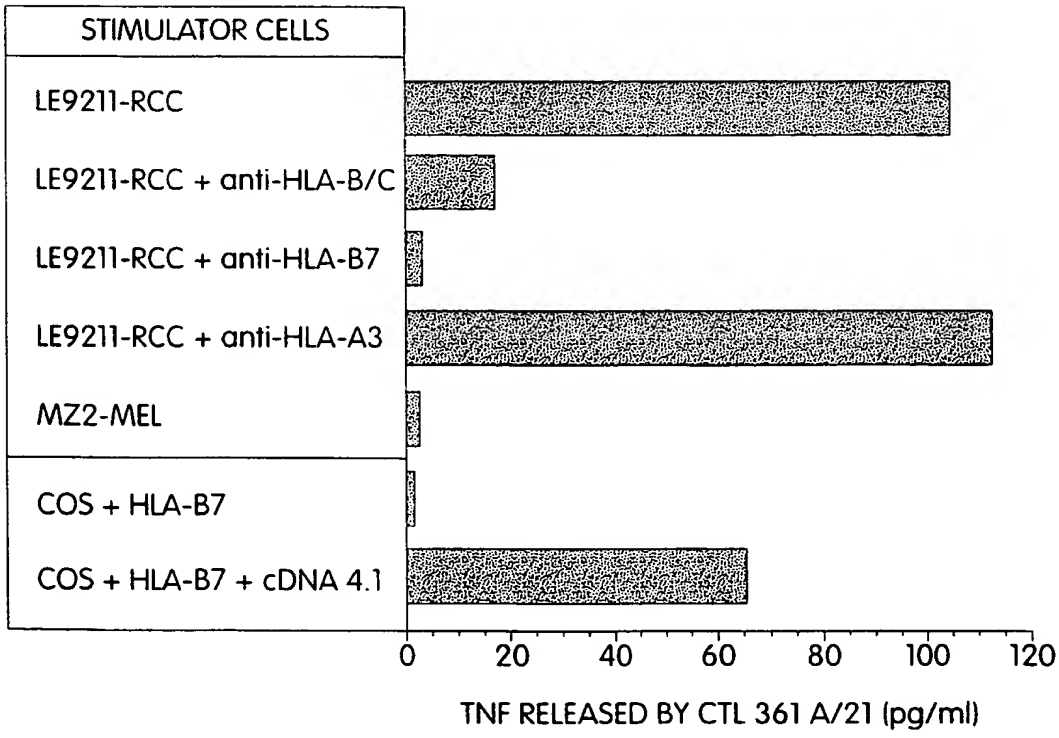
STIMULATOR CELLS
LE9211-RCC
LE9211-RCC + anti-HLA-B/C
LE9211-RCC + anti-HLA-B7
LE9211-RCC + anti-HLA-A3
MZ2-MEL
COS + HLA-B7
COS + HLA-B7 + cDNA 4.1
0 20 40 60 80 100 120
TNF RELEASED BY CTL 361 A/21 (pg/ml)

Fig. 2

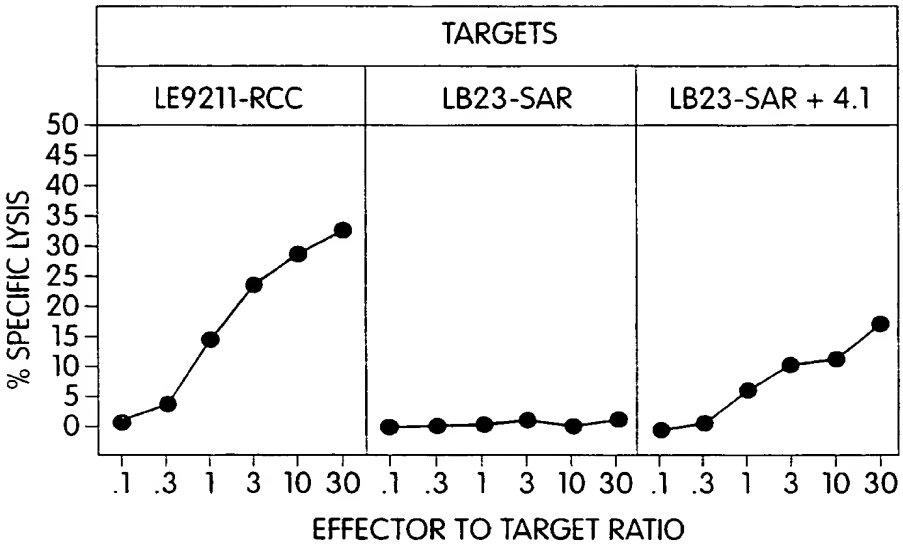
TARGETS
LE9211-RCC
LB23-SAR
LB23-SAR + 4.1
% SPECIFIC LYSIS
50
45
40
35
30
25
20
15
10
5
0
.1 .3 1 3 10 30 .1 .3 1 3 10 30 .1 .3 1 3 10 30
EFFECTOR TO TARGET RATIO

Fig. 3

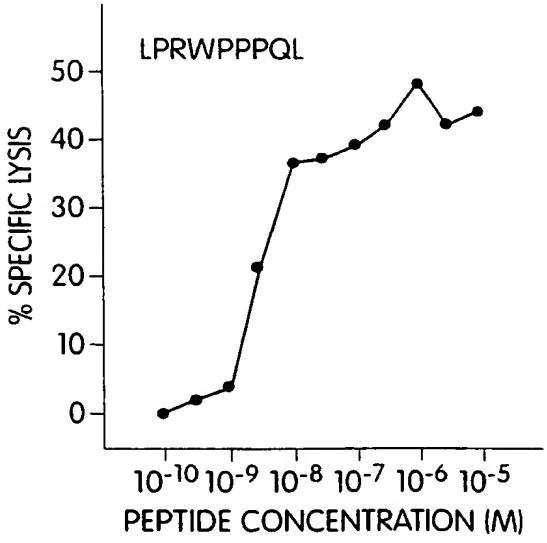
LPRWPPPQL
% SPECIFIC LYSIS
50
40
30
20
10
0
10-10 10-9 10-8 10-7 10-6 10-5
PEPTIDE CONCENTRATION (M)

Fig. 4

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```

GTCCA
6 CCTTGATTCTGCCCGTAGCAGGTGAACCTGGTGTGGTGCGCACTGCGGGTCCTGATTGGCTGTGCACGCCACGGTGAAAAACTTGAGCGTCTACTCCGAGT
109 CCTGCAAGCTCCTAGTGTCTCCTCTGGGTGGACGCCTAGGCGCACGGCCGTTACTTCTCTTTCACCTGTGGATTCGTCAGTTTCTCGTTCGTTTCAGGAGGCG
212 ATCCCGCGCCCTGGGTGCGGTGAGGCCGCTGGGACAGCGGAGGTGCCTCCCGACGCGAAGCAGCTGAGGCGGCGGCCAGCGGGGAAG ATG AGC GGC
M S G
312 AGC AGC GCC AGG TCC AGC CAC CTG TCT CAG CCC GTC GTG AAG AGC GTG CTT GTG TAC CGC AAC GGG GAC CCC TTC TAC
S S A R S S H L S Q P V V K S V L V Y R N G D P F Y
390 GCG GGG CGC CGC GTC GTC ATC CAT GAG AAG AAG GTG TCC AGC TTC GAA GTC TTC CTG AAG GAG GTG ACC GGC GGC GTT
A G R R V V I H E K K K V S S F E V F L K E V T G G V
VDE87
468 CAG GCA CCC TTT GGG GCC GTC AGG AAC ATC TAC ACC CCG CGG ACT GGC CAC CGA ATC CGG AAG CTA GAC CAG ATC CAG
Q A P F G A V R N I Y T P R T G H R I R K L D Q I Q
546 AGC GGG GGC AAT TAC GTG GCT GGA GGC CAG GAA GCC TTC AAG AAA CTC AAT TAC TTG GAC ATA GGA GAA ATC AAG AAA
S G G N Y V A G G Q E A F K K L N Y L D I G E I K K
624 AGA CCA ATG GAA GTT GTT AAT ACA GAG GTA AAA CCA GTA ATC CAT AGC AGG ATC AAC GTG TCA GCT CGC TTT AGA AAA
R P M E V V N T E V K P V I H S R I N V S A R F R K
702 CCG CTT CAG GAG CCG TGC ACT ATC TTC TTG ATT GCA AAT GGA GAC CTC ATA AAC CCA GCT TCT CGC CTC CTT ATC CCC
P L Q E P C T I F L I A N G D L I N P A S R L L I P
VDE93
780 AGA AAA ACC TTG AAT CAG TGG GAT CAT GTA CTA CAA ATG GTC ACA GAA AAA ATC ACT CTG AGG AGC GGG GCT GTT CAC
R K T L N Q W D H V L Q M V T E K I T L R S G A V H
858 AGG CTT TAT ACT TTA GAA GGA AAA CTT GTT GAG AGT GGA GCA GAG TTG GAG AAT GGG CAG TTT TAT GTG GCT GTT GGC
R L Y T L E G K L V E S G A E L E N G Q F Y V A V G
936 AGA GAT AAG TTT AAG AAA CTG CCT TAC GGT GAG TTA CTT TTT GAC AAG TCA ACG ATG AGA AGG CCT TTT GGT CAG AAA
R D K F K K L P Y G E L L F D K S T M R R P F G Q K
1014 GCT TCT TCA CTA CCT CCT CCT ATT GTA GGA TCC AGA AAG TCT AAA GGG AGT GGA AAT GAT CGC CAC TCT AAG TCA ACA GTT
A S S L P P P I V G S R K S K G S G N D R H S K S T V
1092 GGA TCC AGT GAC AAC TCA TCT CCT CAG CCC CTG AAG AGG AAA GGG AAA AAA GAA GAC GTG AAT TCA GAA AAA CTG ACG
G S S D N S S P Q P L K R K G K K E D V N S E K L T

Fig. 6

```
1170  AAA TTG AAA CAA AAT GTA AAA TTA AAG AAT TCA CAA GAA ACC ATT CCA AAT AGT GAT GAA GGC ATT TTC AAA GCT GGA
        K   L   K   Q   N   V   K   L   K   N   S   Q   E   T   I   P   N   S   D   E   G   I   F   K   A   G

1248  GCA GAG AGG TCT GAA ACA CGG GGG GCA GCA GAA GTC CAA GAA GAT GAA GAT ACT CAG GTT GAG GTT CCA GTC GAT CAG
        A   E   R   S   E   T   R   G   A   A   E   V   Q   E   D   E   D   T   Q   V   E   V   P   V   D   Q

1326  AGG CCA GCA GAA ATA GTA GAC GAG GAA GAA GAT GGA GAG AAG GCA AAC AAG GAT GCA GAA CAG AAA GAA GAC TTT TCA
        R   P   A   E   I   V   D   E   E   E   D   G   E   K   A   N   K   D   A   E   Q   K   E   D   F   S

1404  GGA ATG AAT GGT GAC CTT GAA GAG GAA GGA GGT AGG GAG GCT ACA GAT GCC CCT GAG CAA GTC GAG GAG ATT CTG GAT
        G   M   N   G   D   L   E   E   E   G   G   R   E   A   T   D   A   P   E   Q   V   E   E   I   L   D

1482  CAC AGT GAG CAG CAG GCA CGC CCT GCT CGT GTA AAT GGA GGC ACC GAT GAG GAG AAT GGT GAG GAG CTG CAG CAG GTT
        H   S   E   Q   Q   A   R   P   A   R   V   N   G   G   T   D   E   E   N   G   E   E   L   Q   Q   V

1560  AAT AAT GAG CTT CAA CTG GTC CTA GAC AAG GAA AGA AAG TCT CAA GGA GCT GGC AGT GGA CAA GAT GAG GCT GAT GTA
        N   N   E   L   Q   L   V   L   D   K   E   R   K   S   Q   G   A   G   S   G   Q   D   E   A   D   V

1638  GAC CCT CAA AGA CCA CCA AGG CCA GAA GTA AAA ATT ACC AGT CCA GAA GAA AAT GAA AAC AAC CAA CAA AAC AAG GAC
        D   P   Q   R   P   P   R   P   E   V   K   I   T   S   P   E   E   N   E   N   N   Q   Q   N   K   D

1716  TAT GCT GCC GTG GCT TAG AAGATTTTTAAAAAGAGAGTATATGGATCGCAAGAAAAATGAAGGGTTATCATACTTGAAAGATAAGCACATAGTTATT
        Y   A   A   V   A

1813  GCTGAATATAATGTGACACTATGGTCGAATACTACCTACGAATTATAACATTAGAAGCCTAGTGGAAAGACCAGATAACTTTAAATGGCTACTAAAGGATAAT

1914  TACTTACTTTTATTGCATGTGTTTTAAAAGTCATATAGAAATATTAAATAAGACGGACAGAGGAGAATTTGCACTGGAAGACAATTGCCACTTGTAAAGGATG

2019  AAAAATAGGATCACTCTTATTGTACGCTTTATTATAAGTTTAGAAGGCAGTTTATTCTAAATAATTTTTCTCTAGGAAGGCGTAGAATTTTAAAGAACTGGTA

2122  ATAGGAAAGCATGTACTATTTTCTTAAAGCAATAAACTCTTGAATGAAAAAAA
```

Fig. 6 cont.

SUBSTITUTE SHEET (Rule 26)

09/674593

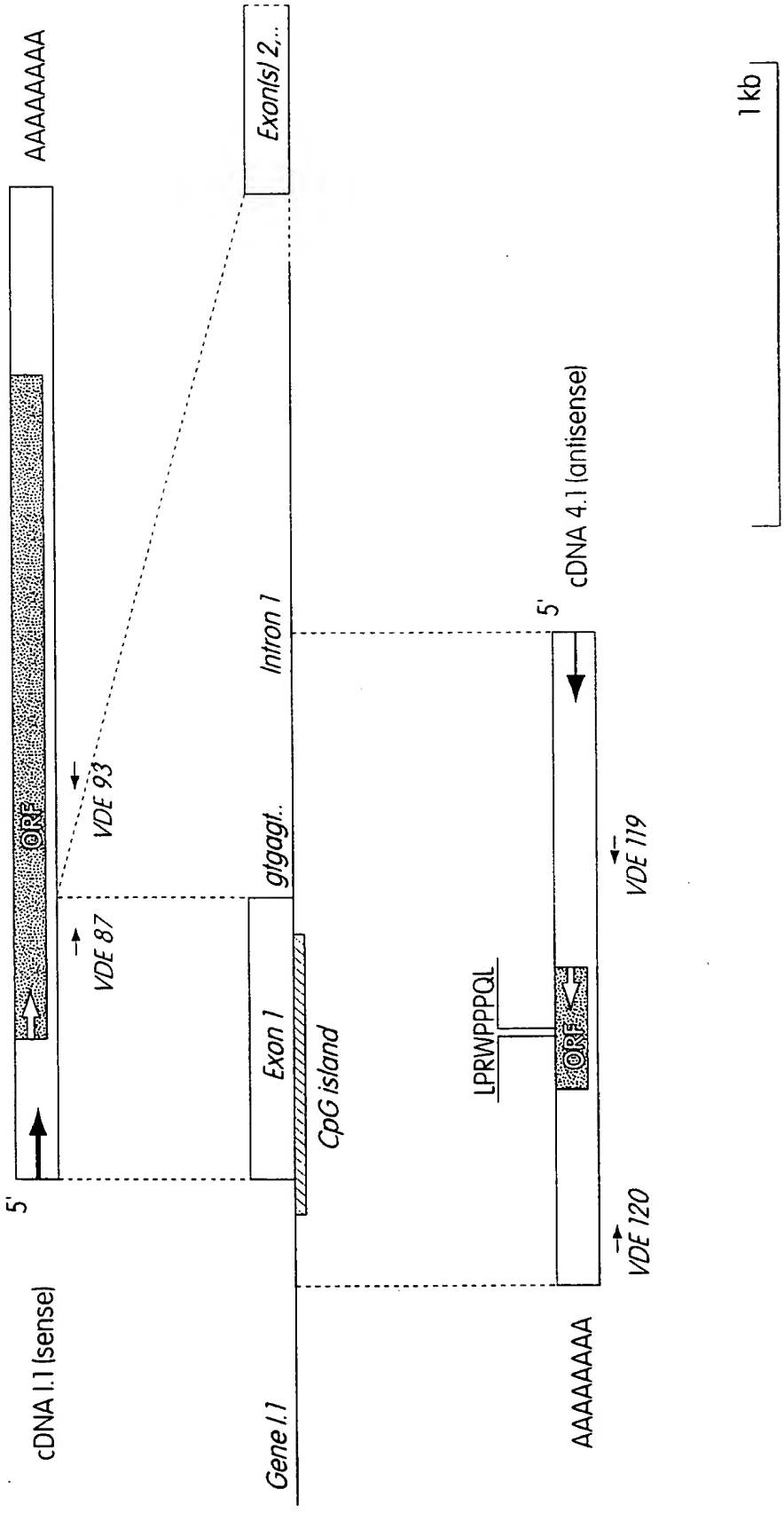
AAAAAAAA
Exon(s) 2,..
ORF
VDE 93
VDE 87
Intron 1
gtgagt..
Exon 1
CpG island
5'
cDNA 1.1 (sense)
Gene 1.1
cDNA 4.1 (antisense)
5'
LPRWPPPQL
ORF
VDE 119
VDE 120
AAAAAAAA
1 kb

Fig. 7

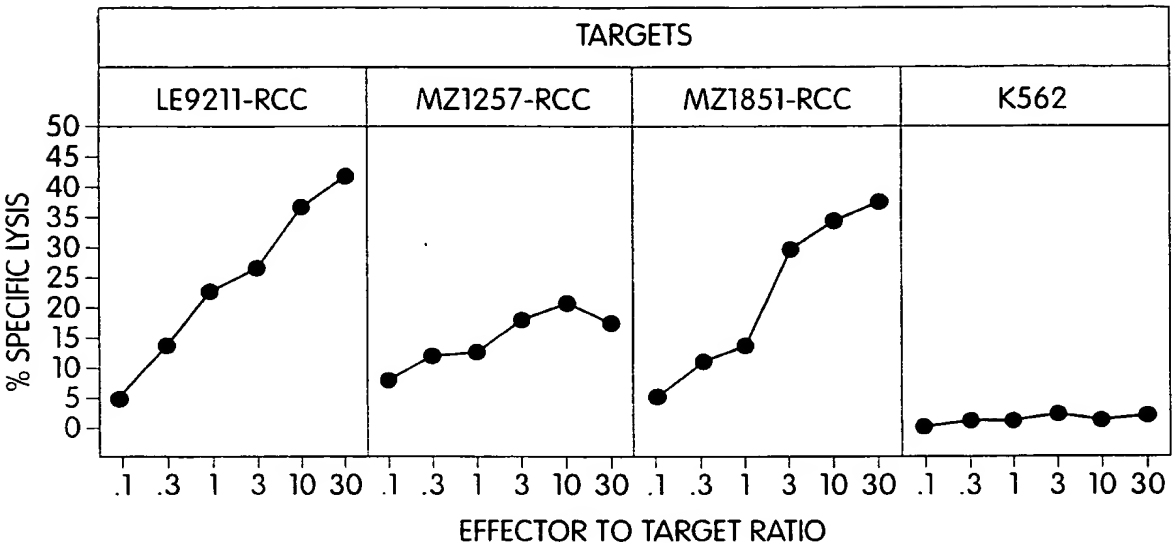
TARGETS
LE9211-RCC
MZ1257-RCC
MZ1851-RCC
K562
% SPECIFIC LYSIS
50
45
40
35
30
25
20
15
10
5
0
.1 .3 1 3 10 30
EFFECTOR TO TARGET RATIO

Fig. 8A

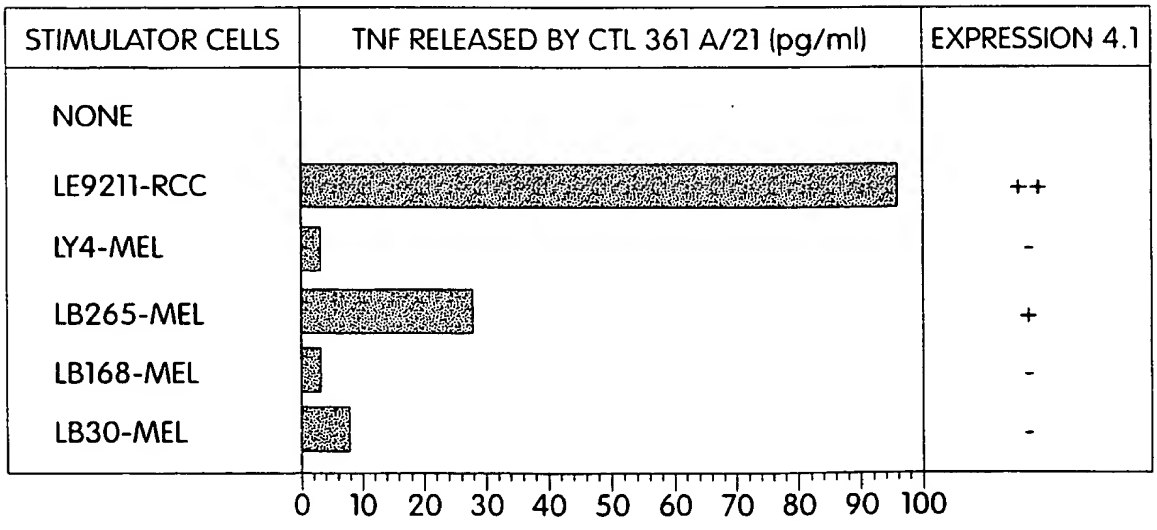
STIMULATOR CELLS
TNF RELEASED BY CTL 361 A/21 (pg/ml)
EXPRESSION 4.1
NONE
LE9211-RCC
LY4-MEL
LB265-MEL
LB168-MEL
LB30-MEL
++
-
+
-
-
0 10 20 30 40 50 60 70 80 90 100

Fig. 8B